

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5
(i) APPLICANT: Chatterjee, Malaya
Foon, Kenneth A.
Chatterjee, Sunil K.

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(ii) TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

(iii) NUMBER OF SEQUENCES: 66

15
(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

30
(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Schiff, J. Michael
(B) REGISTRATION NUMBER: 40,253
(C) REFERENCE/DOCKET NUMBER: 30414-20002.21

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(2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..447

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(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	ATG AAG TTG CCT GTT AGG CTG TTG GTG CTG ATG TTC TGG ATT CCT GCT	48
	Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala	
-19	-15	-10
		-5
15	TCC AGC GAT GAT GTT TTC ATG ACC CAA ACT CCA CTC TCC CTG CCT GTC	96
	Ser Ser Asp Asp Val Phe Met Thr Gln Thr Pro Leu Ser Leu Pro Val	
	1 5 10	
20	AGT CTT GGA GAT CAA GCC TCC ATC TCT TGC AGA TCT AGT CAG AGC ATT	144
	Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile	
	15 20 25	
25	GTA CAT AGT AAT GGA AAC ACC TAT TTA GAA TGG TAC CTA CAG AAA CCA	192
	Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro	
	30 35 40 45	
30	GGC CAG TCT CCA AAC CTC CTG ATC TAC TTT GTT TCC AAC CGA TTT TCT	240
	Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Ser	
	50 55 60	
35	GGG GTC CCA GAC AGG TTC AGT GGC AGT GGA TCA GGG ACA GAT TTC ACA	288
	Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr	
	65 70 75	
40	CTC AAG ATC AGC AGA GTG GAG GCT GAG GAT CTG GGA GTT TAT TAC TGC	336
	Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys	
	80 85 90	
45	TTT CAA GGT TCA CAT GTT CCG TGG ACG TTC GGT GGA GGC ACC AAG CTG	384
	Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly Thr Lys Leu	
	95 100 105	
50	GAA ATC AAA CGG GCT GAT GCA CCA ACT GTA TCC ATC TTC CCA CCA	432
	Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro	
	110 115 120 125	
	TCC AGT AAG CTT GGG	447
	Ser Ser Lys Leu Gly	
	130	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

10 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala
-19 -15 -10 -5

Ser Ser Asp Asp Val Phe Met Thr Gln Thr Pro Leu Ser Leu Pro Val
1 5 10

15 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile
15 20 25

20 Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro
30 35 40 45

Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Ser
50 55 60

25 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr
65 70 75

30 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys
80 85 90

35 Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly Thr Lys Leu
95 100 105

Glut Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
110 115 120 125

Ser Ser Lys Leu Gly
130

40 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..456

5 (ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

10	ATG GCT GTC TTG GGG CTG CTC TTC TGC CTG GTG ACA TTC CCA AGC TGT Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys -19 -15 -10 -5	48
15	GTC CTG TCC CAG GTG CAG GTG AAG GAG TCA GGA CCT TTC CTG GTG CCC Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro 1 5 10	96
20	CCC TCA CAG AGC CTG TCC ATC ACA TGC ACT GTC TCA GGG TTC TCA TTA Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu 15 20 25	144
25	ACC ACC TAT GGT GTA AGC TGG ATT CGC CAG CCT CCA GGA AAG GGT CTG Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu 30 35 40 45	192
30	GAG TGG CTG GGA GCA ATT TGG GGT GAC GGG ACC ACA AAT TAT CAT TCA Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser 50 55 60	240
35	GCT CTC ATA TCC AGA CTG AGC ATC AGC AAG GAT AAC TCC AAG AGC CAA Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln 65 70 75	288
40	GTT TTC TTA AAA CTG AAC AGT CTG CAA ACT GAT GAC ACG GCC ACG TAC Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr 80 85 90	336
45	TAC TGT GCC AAA CTG GGT AAC TAC GAT GCT CTG GAC TAC TGG GGT CAA Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly Gln 95 100 105	384
50	GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC GTC Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro Val 110 115 120 125	432
55	TAT CCA TTG GTC CCT GGA AGC TTG GG Tyr Pro Leu Val Pro Gly Ser Leu 130	458

(2) INFORMATION FOR SEQ ID NO:4:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
-19 -15 -10 -5

10 Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro
1 5 10

Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
15 20 25

15 Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
30 35 40 45

20 Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser
50 55 60

Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln
65 70 75

25 Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr
80 85 90

Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly Gln
95 100 105

30 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro Val
110 115 120 125

35 Tyr Pro Leu Val Pro Gly Ser Leu
130

(2) INFORMATION FOR SEQ ID NO:5:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro Pro Ser Gln
1 5 10 15

50 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Thr Tyr
20 25 30

Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

5 Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser Ala Leu Ile
50 55 60

Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

10 Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr Tyr Cys Ala
85 90 95

Lys Leu

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25 Gly Asn Tyr Asp Ala Leu Asp Trp Trp Gly Gln Gly Thr Ser Val Thr
1 5 10 15

30 Val Ser Ser

30

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr Asp Tyr Glu Xaa Xaa Xaa Xaa Xaa
1 5

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(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1 5

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(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

15

Ser Val Ser Ile Tyr Tyr Tyr Gly Arg Ser Asp Lys
1 5 10

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(2) INFORMATION FOR SEQ ID NO:10:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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Xaa Xaa Xaa Xaa Xaa Xaa
1 5

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(2) INFORMATION FOR SEQ ID NO:11:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

45

Xaa Xaa Xaa Xaa
1

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(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Asp Tyr Arg

1

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Tyr Tyr Asp Xaa

1

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Xaa Xaa Xaa Xaa Xaa

1

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(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly
1 5 10 15

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Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser
20 25 30

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Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Lys Gly Gln Ser
35 40 45

Pro Lys Leu Leu Ile Tyr Phe Val Ser Asn Arg Phe Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
5 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly
85 90 95

10 Ser His Val Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
100 105 110

(2) INFORMATION FOR SEQ ID NO:16:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

25 Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala Pro Ser Gln
1 5 10 15

30 Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu Thr Ser Tyr
20 25 30

Gly Val His Trp Val Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Leu
35 40 45

35 Gly Val Ile Trp Gly Asp Gly Ser Thr Asn Tyr Asn Ser Ala Leu Lys
50 55 60

40 Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln Val Phe Leu
65 70 75 80

45 Lys Met Asn Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr Tyr Cys Ala
85 90 95

Arg Glu Xaa Xaa Xaa Xaa Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
100 105 110

45 Thr Ser Val Thr Val Ser Ser
115

(2) INFORMATION FOR SEQ ID NO:17:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

10 GATGTTTGAGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATACTAATG GAAACACCTA TTTAGAATGG 120
TACCTGCAGAACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAAGTTTC CAACCGATT 180
15 TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTCAC ACTCAAGATC 240
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTTC ACATGTTCCG 300
20 TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAA 336

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

30 GATGTTTGAGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATACTAATG GAAACACCTA TTTAGAATGG 120
TACCTGCAGAACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAAGTTTC CAACCGATT 180
40 TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTCAC ACTCAAGATC 240
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTTC ACATGTTCCG 300
TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAA 336

45 (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5 GATGTTTGA TGACCCAAAC TCCACTCTCC CTNCCTGTCA GTCTTGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATACTAATG GAAACACCTA TTTAGAATGG 120
10 TACCTGCAGA AACCAAGGCCA GTCTCCAAAG CTCCTNATCT ACAAAAGTTTC CAACCGATTT 180
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC 240
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTTC ACATGTTCCG 300
15 TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAA 336

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

20 GATGTTTGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATACTAATG GAAACACCTA TTTAGAATGG 120
TACCTGCAGA AACCAAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAAGTTTC CAACCGATTT 180
30 TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC 240
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTTC ACATGTTCCG 300
35 TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATC 333

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GATGTTTGAGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATACTAATG GAAACACCTA TTTAGAATGG 120
5 TACCTGCAGA AACCCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAAGTTTC CAACCGATTT 180
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTCAC ACTCAAGATC 240
10 AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTTC ACATGTTCC 300
CGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAA 336

(2) INFORMATION FOR SEQ ID NO:22:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 GATGTTGTAGA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATACTAATG GAAACACCTA TTTAGAATGG 120
30 TACCTGCAGA AGCCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAAGTTTC CAACCGATTT 180
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTCAC ACTCAAGATC 240
AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTTC ACATGTTCC 300
35 TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAA 336

(2) INFORMATION FOR SEQ ID NO:23:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

50 GATGTTTGAGA TGACNCAAAC TCCACTCTCC CTGCCTGTCA GTCTTGGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATACTAATG GAAACACCTA TTTAGAATGG 120

TACCTGCAGA AACCAAGGCCA GTCTCCAAAG CTCCTNATCT ACAAAAGTTTC CAACCGATTT 180
TCTGGGGTCC CAGANAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC 240
5 AGCAGAGTGG AGGCTGAGGA TCTGGAGTT TATTACTGCT TTCAAGGTTTC ACATGTTCCG 300
TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAA 336

10 (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 333 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GATGTTTGAA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTGGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120
25 TACCTGCAGA AACCAAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAAGTTTC CAACCGATTT 180
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC 240
AGCAGAGTGG AGGCTGAGGA TCTGGAGTT TATTACTGCT TTCAAGGTTTC ACATGTTCCG 300
30 TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATC 333

35 (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 336 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

45 GATGTTTAA TGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTGGAGA TCAAGCCTCC 60
ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATAGTAATG GAAACACCTA TTTAGAATGG 120
50 TACCTGCAGA AACCAAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAAGTTTC CAACCGATTT 180
TCTGGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTTCAC ACTCAAGATC 240

AGCAGAGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTTC ACATGTTCCG 300

TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAA 336

5 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GATTTTGAGACCCAAAC TCCACTCTCC CTGCCTGTCA GTCTGGAGA TCAAGCCTCC 60

ATCTCTTGCA GATCTAGTCA GAGCATTGTA CATACTAGTG GAAACACCTT TTTAGAATGG 120

TACCTGCAGAACCAGGCCA GTCTCCAAAG CTCCTGATCT ACAAAAGTTTC CAACCGATTT 180

TCTGGGTCC CAGACAGGTT CAGTGGCAGT GGATCAGGGA CAGATTCAC ACTCAAGATC 240

25 AGCAGGGTGG AGGCTGAGGA TCTGGGAGTT TATTACTGCT TTCAAGGTAC ACATGTTCCG 300

TGGACGTTCG GTGGAGGCAC CAAGCTGGAA ATCAA 336

30 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAGGTGCAGCTGCAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60

ACATGCAGTG TCTCAGGGTT CTCATTAACC AGCTATGGTA TAACCTGGGT TCGCCAGCCT 120

45 CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGTG ACGGAAACAC AAATTATCAT 180

TCAGCTCTCA TATCCAGACT GAGCATCAGC AAGGATAACT CCAAGAGCCA AGTTTCTTA 240

50 AAACTGAACA GTCTGCAAAC TGATGACACA GCCACGTACT ACTGTGCCAA A 291

(2) INFORMATION FOR SEQ ID NO:28:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 45 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

10 GCTAAGGACT ACTGGGGTCA AGGAACCTCA GTCACCGTCT CCTCA

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15 (2) INFORMATION FOR SEQ ID NO:29:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

25 CAGGTGCAGC TGAAGGAGAC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC

60

25 ACATGCACCG TCTCAGGGTT CTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT

120

30 CCAGGAAAGG GTCTGGAGTG GCTGGTAGTG ATATGGAGTG ATGGAAGCAC AAACTATAAT

180

30 TCAGCTCTCA AATCCAGACT GAGCATCAGC AAGGACAAC CCAAGAGCCA AGTTTCTTA

240

35 AAAATGAACA GTCTCCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AC

292

35 (2) INFORMATION FOR SEQ ID NO:30:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

50 GGTGACTACT ATGCTATGGA CTACTGGGT CAAGGAACCT CAGTCACCGT CTCCTCA

57

50 (2) INFORMATION FOR SEQ ID NO:31:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs

- (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic).

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

10 CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60
ACATGCACTG TCTCAGGGTT CTCATTAACC AGCTATGGTG TAAGCTGGGT TCGCCAGCCT 120
CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGTG ACGGGAGCAC AAATTATCAT 180
15 TCAGCTCTCA TATCCAGACT GAGCATCAGC AAGGATAACT CCAAGAGCCA AGTTTTCTTA 240
AAACTGAACA GTCTGCAAAC TGATGACACA GCCACGTACT ACTGTGCCAA GCATCTTGAC 300
20 TACTGGGCC AAGGCACCCAC TCTCACAGTC TCCTCA 336

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 304 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

30 CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60
35 ACTTGCACTG TCTCTGGGTT TTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT 120
CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGCTG GTGGAAGCAC AAATTATAAT 180
40 TCGGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAAC CCAAGAGCCA AGTTTTCTTA 240
AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AGGGCATTAC 300
TACG 304

45 (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

5 CTACTATGCT ATGGACTACT GGGGTCAAGG AACCTCAGTC ACCGTCTCC

49

(2) INFORMATION FOR SEQ ID NO:34:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

20 CAGGTGCAGC TCAAGGAGTC AGGACCTGTC CTCGTGGCGC CCTCACAGAG CCTGTCCATC

60

ACTTGCAGTG TCTCTGGTT TTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT

120

CCAGGCAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGCTG GTGGAAGCAC AAATTATAAT

180

25 TCAGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAAC CCAAGAGCCA AGTTTCTTA

240

AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAA AC

292

30 (2) INFORMATION FOR SEQ ID NO:35:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

40 ACAATGCTAT GGACTACTGG GGTCAAGGAA CCTCAGTCAC NGTCTCCTCA

50

(2) INFORMATION FOR SEQ ID NO:36:

45 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CAGGTNCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCAC CCTCACAGAG CCTGTCCATC 60
5 ACATGCACTG TCTCTGGGTT CTCATTATCC AGATATAGTG TACACTGGGT TCGCCAGCCT 120
CCAGGAAAGG GTCTTGAGTG GCTGGGAATG ATATGGGGTG GTGGAAACAC AGACTATAAT 180
10 TCAGCTCTCA AATCCAGACT GAGCATCAGC AAGGACAAC CCAAGAGCCA AGTTTCTTA 240
AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG AGATGGTTAC 300
TACGACTATG CTATGGACTA CTGGGGTCAA GGAACCTCAG TCACCGTCTC C 351

15 (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 291 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60
20 ACTTGCACTG TCTCTGGGTT TTCATTAACC AGCTATGGTG TACACTGGGT TCGCCAGCCT 120
CCAGGAAAGG GTCTGGAGTG GCTGGAGTA ATATGGGCTG GTGGAAGCAC AAATTATAAT 180
30 TCGGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAAC CCAAGAGCCA AGTTTCTTA 240
35 AAAATGAACA GTCTGCAAAC TGATGACACA GCCATGTACT ACTGTGCCAG A 291

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTCC 48
50

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CACGTGCACC	TGAAGGAGTC	AGGACCTGTC	CTGGTGGCGC	CCTCACAGAG	CCTGTCCATC	60
ACTTGCACTG	TCTCTGGTT	TTCATTAACC	AACTATGGTG	TACACTGGGT	TCGCCAGCCT	120
CCAGGAAAGG	GTCTGGAGTG	GCTGGGAGTA	ATATGGGCTG	GTGGAAACAC	AAATTATAAT	180
TCAGCTCTCA	TGTCCAGACT	GAGCATCAGC	AAAGACAATT	CCAAGAGCCA	AGTTTTCTTA	240
AAAATGAACA	GTCTGCAAAT	TGATGACACA	GCCATATACT	ACTGTGCCAA	AC	292

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TACTATGCTA TGGACTATTG GGGTCAAGGA ACCTCAGTC A 51

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

CAGGTGCAGC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60
ACTTGCAC TG TCTCTGGGTT TCCATTAACC AGCTATGGTG TAGACTGGGT TCGCCAGCCT 120
CCAGGAAAGG GTCTGGAGTG GCTGGGAGTA ATATGGGGTG GTGGAAGCAC NAATTATAAT 180

```

TCAGCTCTCA TGTCCAGACT GAGCATCAGC AAAGACAAC CCAAGAGCCA AGTTTCTTA 240

AAAATGAACA GTCTGCNAAC TGATGACACA GCCATGTACT ACTGTGCC 288

5 (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACGGGGNNNTT TACTATGCTA TGGACTACTG GGGTCAAGGA ACCTCAGTCA CCGTCTC 57

20 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CAGGTGCACC TGAAGGAGTC AGGACCTGGC CTGGTGGCGC CCTCACAGAG CCTGTCCATC 60

ACTTGCACTG TCTCTGGATT TTCATTAACC ACCTATGGTG TACACTGGTT TCGCCAGCCT 120

35 CCAGGAAAGG GTCTGGAGTG GCTGGACTA ATATGGGCTG GTGGAAACAC AGATTATAAT 180

TCGGCTCTCA TGTCCAGACT GAGCATCAAC AAAGACAAC CCAAGAGCCA AGTTTCTTA 240

40 AAAATGAACA GTCTGCAAGC TGATGACACA GCCATGTACT ACTGTGCCAG ATT 293

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACGACTATGC TGTGGACTAC TGGGGTCAAG GAACCTCAGT CACCGTCTCC TCA

53

(2) INFORMATION FOR SEQ ID NO:45:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

15

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:46:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
(B) LOCATION: 30
(D) OTHER INFORMATION: /note= "N represents the Nucleotide
Inosine(I)"

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CCCAAGCTTC CAGGGRCCAR KGGATARACN GRTGG

35

35

(2) INFORMATION FOR SEQ ID NO:47:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACTAGTCGAC ATGGCTGTCY TRGBGCTGYT CYTCTG

36

50

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:49:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GTTTTCCCAAG TCACGACGT

19

20 (2) INFORMATION FOR SEQ ID NO:50:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

30 ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCT

39

(2) INFORMATION FOR SEQ ID NO:51:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCCCAAGCTTA CTGGATGGTG GGAAGATGGA

30

(2) INFORMATION FOR SEQ ID NO:52:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CAGATGGAAG GGCCCAAC

18

5 (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GATTGATGCA TATCATTACC

20

15 (2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GTTATCGATG TCGAATAGCC

25

25 (2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGCTGCAGA TTGAGTACTG TTCT

35

40 (2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

50 GCCGATATCA CCATGGCTGT CTTGGGGCTG CTC

33

55 (2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

10 TTGGGTCATC AAAACATCGG ATCCGCCGCC ACCCGAGCCG CCACCGCCCCG AGCCACCTCC 60
CCCTGAGGGAG ACGGTGACTG A 81

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

25 TCAGTCACCG TCTCCTCAGG GGGAGGTGGC TCGGGCGGTG GC GGCTCGGG TGGCGGCCGA 60
TCCGATGTTT TGATGACCCA A 81

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CATCTCTAGA TTATTTGATT TCCAGCTTGG TGCC

40 (2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

50 **GCCGATATCA** CCATGGAGTT GCCTGTTAGG CTG 33

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

10 TGACTCCTTC ACCTGCACCT GGGATCCGCC GCCACCCGAG CCGCCACCGC CCGAGCCACC 60
TCCCCCTTTG ATTTCCAGCT TGGTGCC 87

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GGCACCAAGC TGGAAATCAA AGGGGGAGGT GGCTCGGGCG GTGGCGGCTC GGGTGGCGGC 60
GGATCCCAGG TGCAGGTGAA GGAGTCAG 87

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATCTCTAGA TTATGAGGAG ACGGTGACTG AGGT

34

40 (2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

50 ACCATGG 7

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 13..801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

	GCCGATATCA CC ATG GCT GTC TTG GGG CTG CTC TTC TGC CTG GTG ACA Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr 135 140 145	48
20	TTC CCA AGC TGT GTC CTG TCC CAG GTG CAG GTG AAG GAG TCA GGA CCT Phe Pro Ser Cys Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro 150 155 160	96
25	TTC CTG GTG CCC CCC TCA CAG AGC CTG TCC ATC ACA TGC ACT GTC TCA Phe Leu Val Pro Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser 165 170 175	144
30	GGG TTC TCA TTA ACC ACC TAT GGT GTA AGC TGG ATT CGC CAG CCT CCA Gly Phe Ser Leu Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro 180 185 190	192
35	GGA AAG GGT CTG GAG TGG CTG GGA GCA ATT TGG GGT GAC GGG ACC ACA Gly Lys Gly Leu Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr 195 200 205	240
40	AAT TAT CAT TCA GCT CTC ATA TCC AGA CTG AGC ATC AGC AAG GAT AAC Asn Tyr His Ser Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn 210 215 220 225	288
45	TCC AAG AGC CAA GTT TTC TTA AAA CTG AAC AGT CTG CAA ACT GAT GAC Ser Lys Ser Gln Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp 230 235 240	336
50	ACG GCC ACG TAC TAC TGT GCC AAA CTG GGT AAC TAC GAT GCT CTG GAC Thr Ala Thr Tyr Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp 245 250 255	384
	TAC TGG GGT CAA GGA ACC TCA GTC ACC GTC TCC TCA GGG GGA GGT GGC Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Gly 260 265 270	432
	TCG GGC GGT GGC GGC TCG GGT GGC GGC GGA TCC GAT GTT TTG ATG ACC	480

Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Val Leu Met Thr
275 280 285

5 CAA ACT CCA CTC TCC CTG CCT GTC AGT CTT GGA GAT CAA GCC TCC ATC
 Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
 290 295 300 305

TCT TGC AGA TCT AGT CAG AGC ATT GTA CAT AGT AAT GGA AAC ACC TAT 576
 Ser Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr
 310 315 320

20 AGT GGA TCA GGG ACA GAT TTC ACA CTC AAG ATC AGC AGA GTG GAG GCT 720
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
 355 360 365

25 GAG GAT CTG GGA GTT TAT TAC TGC TTT CAA GGT TCA CAT GTT CCG TGG 768
 Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp
 370 375 380 385

ACG TTC GGT GGA GGC ACC AAG CTG GAA ATC AAA TAATCTAGAG ATG 814
 Thr Phe Gly Gly Thr Lys Leu Glu Ile Lys
 30 390 395

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Met Ala Val Leu Gly Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
1 5 10 15

Val Leu Ser Gln Val Gln Val Lys Glu Ser Gly Pro Phe Leu Val Pro
20 25 30

50 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
35 40 45

Thr Thr Tyr Gly Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu

50 55 60

Glu Trp Leu Gly Ala Ile Trp Gly Asp Gly Thr Thr Asn Tyr His Ser
65 70 75 80

5 Ala Leu Ile Ser Arg Leu Ser Ile Ser Lys Asp Asn Ser Lys Ser Gln
 85 90 95

10 Val Phe Leu Lys Leu Asn Ser Leu Gln Thr Asp Asp Thr Ala Thr Tyr
 100 105 110

15 Tyr Cys Ala Lys Leu Gly Asn Tyr Asp Ala Leu Asp Tyr Trp Gly Gln
 115 120 125

15 Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly
 130 135 140

20 Gly Ser Gly Gly Gly Ser Asp Val Leu Met Thr Gln Thr Pro Leu
 145 150 155 160

20 Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser
 165 170 175

25 Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr
 180 185 190

25 Leu Gln Lys Pro Gly Gln Ser Pro Asn Leu Leu Ile Tyr Phe Val Ser
 195 200 205

30 Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 210 215 220

35 Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly
 225 230 235 240

35 Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly Gly
 245 250 255

40 Gly Thr Lys Leu Glu Ile Lys
 260